



All ENCODE data can be visualized in the UCSC Genome Browser as annotation tracks.

Signals detected in experiments can be shown in various modes. Dense mode compresses data into the most compact display style. Choosing other visibility types may provide further details. Full display offers the most expanded view of the underlying data, with additional graphical details that can provide signal histogram and designations of the "peak" locations.

ENCODE tracks can be found in many track groups. Hyperlinks provide access to track details, sometimes as a super-track page for a set, or to individual subtracks for specific technique and experimental details and filter options.

ENCODE data are identified in the browser annotation track menu by the NHGRI helix icon symbol

**ENCODE Regulation Super-track Settings**

**Integrated Regulation from ENCODE Tracks** (+All Regulation tracks)

Display mode: show [Submit]

- All
- Transcription Transcription Levels Assayed by RNA-seq on 9 Cell Lines from ENCODE
- Layered H3K4Me1 H3K4Me1 Mark (Often Found Near Regulatory Elements) on 7 cell lines from ENCODE
- Layered H3K4Me3 H3K4Me3 Mark (Often Found Near Promoters) on 7 cell lines from ENCODE
- full Layered H3K27Ac H3K27Ac Mark (Often Found Near Active Regulatory Elements) on 7 cell lines from ENCODE
- DNase Clusters Digital DNase Hypersensitivity Clusters from ENCODE
- Txn Factor ChIP Transcription Factor ChIP-seq from ENCODE

NOTE: Early access to additional track data may be available on the [Preview Browser](#).

**Description**

These tracks display information relevant to the regulation of transcription from the ENCODE project. The Transcription track shows transcription levels assayed by sequencing of polyadenylated RNA from a variety of cell types. The Overlaid H3K4Me1 and Overlaid

ENCODE Regulation super-track is an integrated collection of related data types that can help researchers evaluate a genomic region. Transcription levels, histone marks, chromatin state and transcription factor binding can be quickly displayed.

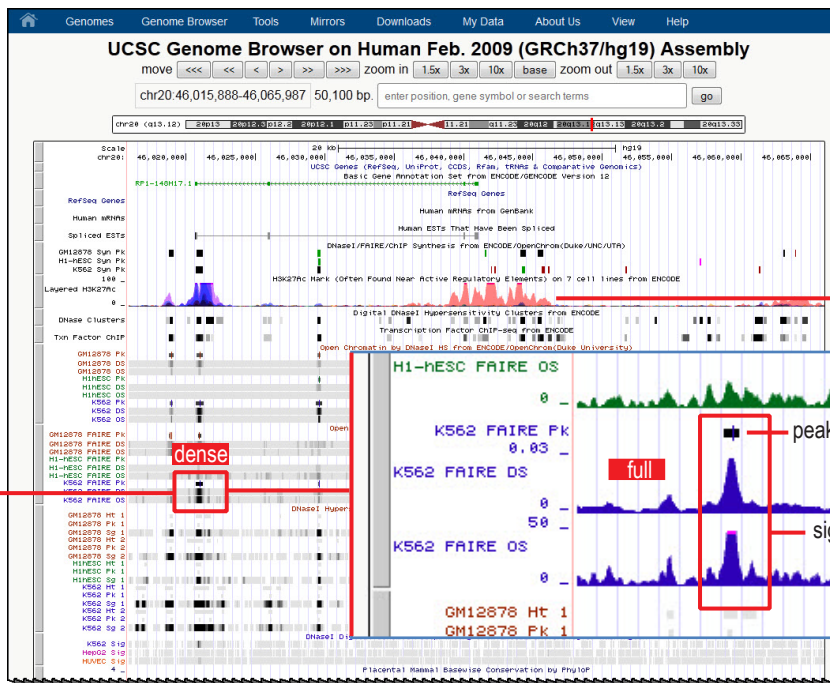
List subtracks: only selected/visible all (7 of 7 selected) Restricted Until

- GM12878 H3K27Ac Mark (Often Found Near Regulatory Elements) on GM12878 Cells from ENCODE - schema 2009-10-05
- H1-hESC H3K27Ac Mark (Often Found Near Regulatory Elements) on H1-hESC Cells from ENCODE - schema 2011-03-21
- HSM1 H3K27Ac Mark (Often Found Near Regulatory Elements) on HSM1 Cells from ENCODE - schema 2010-09-16
- HUVEC H3K27Ac Mark (Often Found Near Regulatory Elements) on HUVEC Cells from ENCODE - schema 2009-10-06
- K562 H3K27Ac Mark (Often Found Near Regulatory Elements) on K562 Cells from ENCODE - schema 2009-10-05
- NHEK H3K27Ac Mark (Often Found Near Regulatory Elements) on NHEK Cells from ENCODE - schema 2009-10-07
- NHLF H3K27Ac Mark (Often Found Near Regulatory Elements) on NHLF Cells from ENCODE - schema 2010-06-28

Principal Investigator on grant: Bernstein  
Lab producing data: Bernstein - Broad Institute  
Experiment (Assay) type: ChIP-seq  
View - Peaks or Signals: Signal  
Cell, tissue or DNA sample: NHLF  
Treatment: None  
Antibody or target protein: H3K27Ac (ab47)  
Control or Input for ChIP-seq: Standard Control  
Assembly originally mapped to: hg18  
ENCODE Data Freeze: ENCODE Jan 2  
UCSC Accession: wgEncodeahg18  
Date submitted to UCSC: 2009-09-29  
Date resubmitted to UCSC: 2010-11-05  
Date restrictions end: 2010-06-28  
Submission ID: 2916  
GEO sample accession: GSM733646  
Experiment or input: exp  
Control - explicit relationship: NHLF InputStd  
labelName: wgEncodeBroadHistoneNHLF H3K27Ac SId5lg  
fileName: wgEncodeBroadHistoneNHLF H3K27Ac SId5lg bigwig

Click on triangle to access meta-data for further details about the experimental scenario and contributing team.

For some tracks, individual cell line signals will be viewed as histogram displays. Users can show or hide specific cell lines of interest by selecting them.



ENCODE data can be visualized and queried like any other data in the UCSC Genome Browser, across the entire genome. For help with an overview of the UCSC foundations, see the OpenHelix tutorials that provide more background.

This "wiggle" track display shows the signal level in various cell lines (identified by color) which can be turned on and off (see below)

Tracks have different conventions and color codes, but many will offer both signal displays of the full results across a region, and also show a peak value in that region as well. Some tracks will offer filters to set threshold values.

**Regulation** refresh

- ENCODE Regulation... show
- CD34 Dnasel hide
- CpG Islands hide
- ENC Chromatin... hide
- ENC DNA Methy... hide
- ENC DNase/FAIRE... show
- ENC Histone... hide
- ENC RNA Binding... hide
- ENC TF Binding... hide
- FSU Repli-chip hide
- OReqAnno hide
- Slaf Nucleosome hide

Super-tracks combine related topic data using different techniques (such as open chromatin state here) that can be evaluated together.

**ENC DNase/FAIRE Super-track Settings**

**ENCODE Open Chromatin by DNaseI HS and FAIRE Tracks** (+All Regulation tracks)

Display mode: show [Submit]

- dense Open Chrom Synth DNaseI/FAIRE/ChIP Synthesis from ENCODE/OpenChrom(Duke/UNC/UTA)
- dense Duke DNaseI HS Open Chromatin by DNaseI HS from ENCODE/OpenChrom(Duke University) Through the ENCODE July 2012 Freeze
- dense UNC FAIRE Open Chromatin by FAIRE from ENCODE/OpenChrom(UNC Chapel Hill) through the ENCODE Jan 2011 Freeze
- dense UW DNaseI HS DNaseI Hypersensitivity by Digital DNaseI from ENCODE/University of Washington
- dense UW DNaseI LGF DNaseI Digital Genomic Footprinting from ENCODE/University of Washington

NOTE: Early access to additional track data may be available on the [Preview Browser](#).

**Description**

These tracks display ev accessible to the regula inaccessible. Transcription

Open chromatin was ide Elements FAIRE) 300

**ENC FAIRE Track Settings**

**Open Chromatin by FAIRE from ENCODE/ OpenChrom(UNC Chapel Hill)**

Maximum display mode: dense [Submit] Ca full 1 to defaults

Select views (help):  
Peaks: dense Density Signal full Overlap Signal full

Select subtracks by treatment and cell line:

Cell Line	Treatment	None	Hypoxia	IFN&alpha	IFN&gamma	Sodium	UT189
GM12878 (Tier 1)		<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
H1-hESC (Tier 1)		<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
K562 (Tier 1)		<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
HeLa-S3 (Tier 2)		<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
HepG2 (Tier 2)		<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
HUVEC (Tier 2)		<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
GM12891	A549	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
GM12892	Gliobla	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
GM18507		<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>

Users can choose various aspects of the experiments to display. Peaks, signals, individual cell lines, replicates, and various treatment conditions may be available to select and explore.

Super-track and track Description sections will have crucial meta-data to understand the projects, and will explain the display conventions, color codes, and more. Citations for data or technologies may be provided when available. Credits and contacts for the project teams will also be provided.

visit [www.openhelix.com/ENCODE2](http://www.openhelix.com/ENCODE2) for ENCODE tutorials and training materials

[www.openhelix.com](http://www.openhelix.com)  
or call 1-888-861-5051